WE CLAIM:

1. An isolated polynucleotide from coryneform bacteria, comprising a polynucleotide sequence which codes for the cstA gene, selected from the group consisting of

   a) a polynucleotide which is identical to the extent of at least 70% to a polynucleotide which codes for a polypeptide which comprises the amino acid sequence of SEQ ID No. 2,

   b) a polynucleotide which codes for a polypeptide which comprises an amino acid sequence which is identical to the extent of at least 70% to the amino acid sequence of SEQ ID No. 2,

   c) a polynucleotide which is complementary to the polynucleotides of a) or b), and

   d) a polynucleotide comprising at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c).

2. The polynucleotide according to claim 1, wherein the polypeptide of a) or b) has the activity of carbon starvation protein A.

3. The polynucleotide according to claim 1, wherein the polynucleotide is a recombinant DNA which is capable of replication in coryneform bacteria.

4. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.

5. The polynucleotide according to claim 3, comprising the nucleic acid sequence as shown in SEQ ID No. 1.

6. The polynucleotide according to claim 3, wherein polynucleotide is a DNA which is capable of replication, comprising

(i) the nucleotide sequence shown in SEQ ID No. 1, or

(ii) at least one sequence which corresponds to sequence (i) within the range of the degeneration of the genetic code, or

(iii) at least one sequence which hybridizes with the sequence complementary to sequence (i) or (ii).

7. The polynucleotide according to claim 6, further comprising

(iv) sense mutations of neutral function in (i).

8. The polynucleotide sequence according to claim 3, which codes for a polypeptide which comprises the amino acid sequences shown in SEQ ID No. 2.

9. A coryneform bacteria in which the cstA gene is enhanced.

10. The coryneform bacteria according to claim 9, wherein the cstA gene is over-expressed.

11. A shuttle vector Escherichia coli DH5alphamcr/pEC-K18mob2cstAexp deposited as DSM 13671.

12. A method for the fermentative preparation of L-amino acids in coryneform bacteria, comprising:

a) fermenting, in a medium, the coryneform bacteria which produce the desired L-amino acid and in which at least the cstA gene or nucleotide sequences which code for it are enhanced.

13. The method according to claim 12, further comprising

b) concentrating the L-amino acid in the medium or in the cells of the bacteria.

14. The method according to claim 13, further comprising

c) isolating the L-amino acid.

15. The method according to claim 12, wherein the L-amino acids are L-lysine.

16. The method according to claim 12, wherein at least the cstA gene or nucleotide sequences which code for it are over-expressed.

17. The method according to claim 12, wherein the bacteria comprise additional genes of the biosynthesis pathway of the desired L-amino acid are enhanced.

18. The method according to claim 12, wherein bacteria in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partly eliminated are employed.

19. The method according to claim 12, wherein a strain transformed with a plasmid vector is employed, and the plasmid vector carries the nucleotide sequence which codes for the cstA gene.

20. The method according to claim 12, wherein the expression of the polynucleotide which codes for the cstA gene is enhanced.

21. The method according to claim 20, wherein the expression of the polynucleotide which codes for the cstA gene is over-expressed.

22. A method according to claim 12, wherein the regulatory properties of the polypeptide for which the polynucleotide cstA codes are increased.

23. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more

genes which are enhanced; wherein the one or more genes is/are selected from the group consisting of:

the lysC gene which codes for a feed back resistant aspartate kinase,

the dapA gene which codes for dihydrodipicolinate synthase,

the gap gene which codes for glycerolaldehyde 3-phosphate dehydrogenase,

the pgk gene which codes for 3-phosphoglycerate kinase,

the pyc gene which codes for pyruvate carboxylase,

the tpi gene which codes for triose phosphate isomerase,

the lysE gene which codes for lysine export, and

the zwa1 gene which codes for the Zwa1 protein.

24. The method according to claim 23, wherein the one or more genes are overexpressed.

25. The method according to claim 12, wherein the bacteria being fermented comprise, at the same time, one or more genes which are attenuated; wherein the one or more genes is/are selected from the group consisting of:

the pck gene which codes for phosphoenol pyruvate carboxykinase,

the pgi gene which codes for glucose 6-phosphate isomerase,

the poxB gene which codes for pyruvate oxidase, and

the zwa2 gene which codes for the Zwa2 protein.

26. The method according to claim 12, wherein microorganisms of the genus Corynebacterium glutamicum are employed.

27. A Coryneform bacteria comprising a vector which carries a polynucleotide according to claim 1.

28. A method for discovering RNA, cDNA and DNA in order to isolate nucleic acids, or polynucleotides or genes which code for carbon starvation protein A or have a high similarity with the sequence of the cstA gene, comprising contacting the RNA, cDNA, or DNA with hybridization probes comprising polynucleotide sequences according to claim 1.

29. The method according to claim 28, wherein the hybridization is carried out under a stringency corresponding to at most 2x SSC.

30. The method according to claim 28, wherein arrays, micro arrays or DNA chips are employed.